



## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/798,790  
Source: JFW  
Date Processed by STIC: 8/11/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

~~TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER~~  
~~VERSION 4.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND~~  
~~TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:~~

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>) , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box-1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04):  
U.S. Patent and Trademark Office, 220 20<sup>th</sup> Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202

## Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	SERIAL NUMBER: <u>10/298,790</u>
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ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics  
    Wrapped Aminos     The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
  
- 2      Invalid Line Length     The rules require that a line **not exceed** 72 characters in length. This includes white spaces.
  
- 3      Misaligned Amino  
    Numbering     The numbering under each 5<sup>th</sup> amino acid is misaligned. **Do not use tab codes between numbers; use space characters**, instead.
  
- 4      Non-ASCII     The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**
  
- 5      Variable Length     Sequence(s)          contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
  
- 6      PatentIn 2.0  
    "bug"     A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)         . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
  
- 7      Skipped Sequences     Sequence(s)          missing. If intentional, please insert the following lines for **each** skipped sequence:  
     (OLD RULES): (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                   (i)      SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
                   (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                   This sequence is intentionally skipped  
  
     Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
  
- 8      Skipped Sequences     Sequence(s) 5 missing. If intentional, please insert the following lines for **each** skipped sequence.  
     (NEW RULES)     <210> sequence id number  
                     <400> sequence id number  
                     000  
                     *← This is the only valid format.*
  
- 9      Use of n's or Xaa's  
    (NEW RULES)     Use of n's and/or Xaa's have been detected in the Sequence Listing.  
                     Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.  
                     In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
  
- 10      Invalid <213>  
    Response     Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence
  
- 11      Use of <220>     Sequence(s)          missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is **MANDATORY** if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
                     (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
  
- 12      PatentIn 2.0  
    "bug"     Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
  
- 13      Misuse of n/Xaa     "**n**" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



IFWO

## RAW SEQUENCE LISTING

DATE: 08/11/2004

PATENT APPLICATION: US/10/798,790

TIME: 16:21:30

Input Set : A:\REL4-2US.ST25.txt

Output Set: N:\CRF4\08112004\J798790.raw

3 <110> APPLICANT: Totey, Satish  
 4 Ravindran, Geeta  
 6 <120> TITLE OF INVENTION: DERIVATION OF TERMINALLY DIFFERENTIATED DOPAMINERGIC NEURONS  
 FROM  
 7 HUMAN EMBRYONIC STEM CELLS  
 9 <130> FILE REFERENCE: REL494/4-002US  
 11 <140> CURRENT APPLICATION NUMBER: 10/798,790  
 12 <141> CURRENT FILING DATE: 2004-03-11  
 14 <150> PRIOR APPLICATION NUMBER: 269/Mum/2003  
 15 <151> PRIOR FILING DATE: 2003-03-12  
 17 <150> PRIOR APPLICATION NUMBER: 60/520,048  
 18 <151> PRIOR FILING DATE: 2003-11-14  
 20 <160> NUMBER OF SEQ ID NOS: 12  
 22 <170> SOFTWARE: PatentIn version 3.3

## ERRORED SEQUENCES

60 <210> SEQ ID NO: 5  
 61 <211> LENGTH: 0  
 62 <212> TYPE: DNA  
 63 <213> ORGANISM: Homo sapiens  
 65 <400> SEQUENCE: 5  
 E--> 65 5

Does Not Comply  
 Corrected Diskette Needed

see P.2

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2

<210> 5  
<211> 0  
<212> DNA  
<213> Homo sapiens

<400> 5  
<210> 6

If this is an intentionally skipped sequence, please use the format shown in item 8 on Error Summary Sheet

**VERIFICATION SUMMARY**

PATENT APPLICATION: US/10/798,790

DATE: 08/11/2004

TIME: 16:21:32

Input Set : A:\REL4-2US.ST25.txt

Output Set: N:\CRF4\08112004\J798790.raw

L:65 M:301 E: (44) No Sequence Data was Shown, SEQ ID:5